

*Exhibit D***Blast 2 Sequences results**

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Entrez

BLAST

OMIM

Taxonomy

Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]**

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☒ View option **Standard**  
Masking character option **X for protein, n for nucleotide** Masking color option **Black**  
☐ Show CDS translation **Align**

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**Sequence 1:** lcl|seq\_1

Length = 14

**Sequence 2:** lcl|seq\_2

Length = 31

**No significant similarity was found**

CPU time: 0.01 user secs. 0.01 sys. secs 0.02 total secs.

Lambda	K	H
0.334	0.138	0.589

**Gapped**

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 7

Number of extensions: 4

Number of sequences better than 10.0: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Length of query: 14

Length of database: 1,129,354,045

Length adjustment: 0

Effective length of query: 14

Effective length of database: 1,129,354,045

Effective search space: 15810956630

Effective search space used: 15810956630

Neighboring words threshold: 9

X1: 15 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 39 (21.7 bits)

S2: 68 (30.8 bits)